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CHRISTENSON, STEVEN D.
STANDAGE, SCOTT

<120> GENE CLUSTER FOR PRODUCTION OF THE ENEDIYNE ANTITUMOR ANTIBIOTIC C-1027

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Met Arg Met Leu Val
1 5

acg ggc gga gcg ggt ttc atc ggc tcg cag ttc gtg cgg gcc aca ctg 163
Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln Phe Val Arg Ala Thr Leu
10 15 20

cac ggc gag ctg ccg ggt tcc gag gac gcc cgg gtg acg gtc ctg gac 211
His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg Val Thr Val Leu Asp
25 30 35

aag ctg acg tac tcc ggc aat ccg gcc aac ctc acc tcc gtc gcg gcc 259
Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu Thr Ser Val Ala Ala
40 45 50

cat ccg cgg tac acc ttc gtc cag ggc gac acc gtc gac ccg cgc gtc 307
His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr Val Asp Pro Arg Val
55 60 65

gtc gac gag gtg gtc gcc ggc cac gac gtc atc gtc cac ttc gcg gcg 355
Val Asp Glu Val Val Ala Gly His Asp Val Ile Val His Phe Ala Ala
70 75 80 85

gag tcg cac gtg gac cgc tcg atc gac acc gcc acc cgg ttc gtc acg 403
Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala Thr Arg Phe Val Thr
90 95 100

acc aac gtg ctc ggg acc cag acg ctg ctg gaa gcg gct ctc cgg cac 451

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ggg gtc ggc cgg ttc gtg cac gtg tcg acc gac gag gtc tac ggg tcg   499
Gly Val Gly Arg Phe Val His Val Ser Thr Asp Glu Val Tyr Gly Ser
        120                 125                 130

atc gcc tcc ggc tca tgg acc gag gac acc ccg ctc gcc ccc aac gtc   547
Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro Leu Ala Pro Asn Val
    135                 140                 145

ccc tac gcg gcg tcg aag gcg ggt tcg gac ctg atg gcg ctc gcc tgg   595
Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu Met Ala Leu Ala Trp
150                 155                 160                 165

cac cgc acc cgg ggc ctg gac gtc gtc gtc acc cgg tgc acc aac aac   643
His Arg Thr Arg Gly Leu Asp Val Val Val Thr Arg Cys Thr Asn Asn
                170                 175                 180

tac ggt ccc tac cag tac ccc gag aag gtg atc ccg ctc ttc gtc acc   691
Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile Pro Leu Phe Val Thr
            185                 190                 195

aac atc ctc gac ggc ttg cgg gtg ccc ctg tac ggg gac ggc gcc cac   739
Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr Gly Asp Gly Ala His
        200                 205                 210

cgc cgg gac tgg ctg cac gtg tcc gac cac tgc cgg gcc atc cag atg   787
Arg Arg Asp Trp Leu His Val Ser Asp His Cys Arg Ala Ile Gln Met
    215                 220                 225

gtc atg aac tcc ggc cgg gcc ggg gag gtc tac cac atc ggc ggc ggc   835
Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr His Ile Gly Gly Gly
230                 235                 240                 245

acc gaa ctc tcc aac gag gaa ctc acc ggc ctg ttg ctc acg gcg tgc   883
Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu Leu Leu Thr Ala Cys
                250                 255                 260

ggc acc gac tgg tcc tgc gtg gac cgg gtg gcc gac cgg cag ggg cac   931
Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala Asp Arg Gln Gly His
            265                 270                 275

gac cgc cgc tac tcg ctc gac atc acg aag atc cgg cag gaa ctg ggc   979
Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile Arg Gln Glu Leu Gly
        280                 285                 290

tac gag ccc ctg gtc gcc ttc gag gac ggc ctg gcc gcg acg gtg aag   1027
Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu Ala Ala Thr Val Lys
    295                 300                 305

tgg tac cac gag aac cgt tcg tgg tgg cag ccg ctg aag gaa gcg gcc   1075
Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro Leu Lys Glu Ala Ala
310                 315                 320                 325

ggc ctc ctg gac gcc gtc ggc tgacggcagc caccgctagg aacaccccag      1126
Gly Leu Leu Asp Ala Val Gly
                330

gaaaggagcc acctcc gtg aca gca gtc aag gag ccg acg tcc cgc gca gga 1178
                  Met Thr Ala Val Lys Glu Pro Thr Ser Arg Ala Gly
                      335                 340

cgg cgg gag tgg atc gct ctc gtc gtc ctc tcc ttg ccc acg atg ctg   1226
```

D8 Cont.

```
Arg Arg Glu Trp Ile Ala Leu Val Val Leu Ser Leu Pro Thr Met Leu
345                 350                 355                 360

ttg atg ctg gac atc aac gtc ctc atg ctg gcc ttg ccg cag ttg agc   1274
Leu Met Leu Asp Ile Asn Val Leu Met Leu Ala Leu Pro Gln Leu Ser
                365                 370                 375

gag gat ctc ggc gcg agc agc acg caa cag ctg tgg atc acc gac atc   1322
Glu Asp Leu Gly Ala Ser Ser Thr Gln Gln Leu Trp Ile Thr Asp Ile
            380                 385                 390

tac gga ttc gcg atc gcc ggc ttc ctg gtg acc atg ggc acc ctc ggc   1370
Tyr Gly Phe Ala Ile Ala Gly Phe Leu Val Thr Met Gly Thr Leu Gly
        395                 400                 405

gac cgg atc ggc cgc cgc agg ctc ctg ctc ggg ggc gcg gcc gtc ttc   1418
Asp Arg Ile Gly Arg Arg Arg Leu Leu Leu Gly Gly Ala Ala Val Phe
    410                 415                 420

gcg gtc gtg tcc gtc gtc gcc gcg ttc tcc gac agc gcg gcg atg ctc   1466
Ala Val Val Ser Val Val Ala Ala Phe Ser Asp Ser Ala Ala Met Leu
425                 430                 435                 440

gtc gtc agc cgc gcc gtg ctc ggc gtc gcc ggg gcc acg gtg atg ccc   1514
Val Val Ser Arg Ala Val Leu Gly Val Ala Gly Ala Thr Val Met Pro
                445                 450                 455

tcg acg ctc gcg ctc atc agc aac atg ttc gag gac ccc aag gag cgg   1562
Ser Thr Leu Ala Leu Ile Ser Asn Met Phe Glu Asp Pro Lys Glu Arg
            460                 465                 470

ggc acc gcc atc gcc atg tgg gcg agc gcc atg atg gcc gga gtc gcc   1610
Gly Thr Ala Ile Ala Met Trp Ala Ser Ala Met Met Ala Gly Val Ala
        475                 480                 485

ctc ggg ccc gcc gtc ggc ggc ctg gtc ctc gcc gcg ttc tgg tgg gga   1658
Leu Gly Pro Ala Val Gly Gly Leu Val Leu Ala Ala Phe Trp Trp Gly
    490                 495                 500

tcg gtg ttc ctc atc gcc gtt ccg gtg atg ctg ctg gtg gtg gtc acc   1706
Ser Val Phe Leu Ile Ala Val Pro Val Met Leu Leu Val Val Val Thr
505                 510                 515                 520

ggc ccc gtg ctg ctc acc gag tcc cgc gac ccg gac gcc gga cgg ctg   1754
Gly Pro Val Leu Leu Thr Glu Ser Arg Asp Pro Asp Ala Gly Arg Leu
                525                 530                 535

gac ctg ctg agc gcg ggg ctc tcc ctc gcg acc gtg ctg ccg gtg atc   1802
Asp Leu Leu Ser Ala Gly Leu Ser Leu Ala Thr Val Leu Pro Val Ile
            540                 545                 550

tac gga ctg aag gag ctg gcc cgg acc ggg tgg gac ccg ctc gcc gcc   1850
Tyr Gly Leu Lys Glu Leu Ala Arg Thr Gly Trp Asp Pro Leu Ala Ala
        555                 560                 565

ggc gcg gtg gtc ctc ggc gtg atc ttc ggc gcg ctg ttc gtc cag cgc   1898
Gly Ala Val Val Leu Gly Val Ile Phe Gly Ala Leu Phe Val Gln Arg
    570                 575                 580

cag cgg cgg ttg gcc gac ccc atg ctg gac ctc ggc ctc ttc gcc gac   1946
Gln Arg Arg Leu Ala Asp Pro Met Leu Asp Leu Gly Leu Phe Ala Asp
585                 590                 595                 600
```

D8 Cont

```
cgc acc ctg cgg gcg ggt ctg acg gtc agt ctg gtc aac gcc gtc atc   1994
Arg Thr Leu Arg Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile
                605                 610                 615

atg ggc ggg acc gga ctg atg gtc gcc ctg tac ctc cag acg atc gcc   2042
Met Gly Gly Thr Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala
            620                 625                 630

ggt cac tcc ccg ttg gcc gcc ggg ctg tgg ctg ctg atc ccg gcc tgc   2090
Gly His Ser Pro Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys
        635                 640                 645

atg ctc gtc gtg ggc gta cag ctg tcg aac ctg ctg gcc cag cgg atg   2138
Met Leu Val Val Gly Val Gln Leu Ser Asn Leu Leu Ala Gln Arg Met
    650                 655                 660

ccc cct tcc cgg gtg ctg ctg ggg gga ctg ctg atc gcg gcc gtc gga   2186
Pro Pro Ser Arg Val Leu Leu Gly Gly Leu Leu Ile Ala Ala Val Gly
665                 670                 675                 680

cag ctc ctg atc acc cag gtg gac acc gag gac acc gcc ctc ctc atc   2234
Gln Leu Leu Ile Thr Gln Val Asp Thr Glu Asp Thr Ala Leu Leu Ile
                685                 690                 695

gcg gcc acc acc ctg atc tac ttc ggc gcc tca ccg gtg ggg ccg atc   2282
Ala Ala Thr Thr Leu Ile Tyr Phe Gly Ala Ser Pro Val Gly Pro Ile
            700                 705                 710

acc acg ggc gcg atc atg gga gcc gcg ccc ccg gag aag gcg ggt gcc   2330
Thr Thr Gly Ala Ile Met Gly Ala Ala Pro Pro Glu Lys Ala Gly Ala
        715                 720                 725

gcc tcg tcg ctg tcc gcc acc ggc ggc gag ttc gga gtg gcg ctc ggc   2378
Ala Ser Ser Leu Ser Ala Thr Gly Gly Glu Phe Gly Val Ala Leu Gly
    730                 735                 740

atc gcg ggc ctg ggg agt ctg ggc acc gtc gtg tac agc gcc ggg gtc   2426
Ile Ala Gly Leu Gly Ser Leu Gly Thr Val Val Tyr Ser Ala Gly Val
745                 750                 755                 760

gag gtg ccg gac gcg gcc ggg ccc gcc gac gcc gac gcc gcg cag gag   2474
Glu Val Pro Asp Ala Ala Gly Pro Ala Asp Ala Asp Ala Ala Gln Glu
                765                 770                 775

agc atc gcc ggc gcc ctg cac acg gcc ggt cag ctg gca ccg ggc agc   2522
Ser Ile Ala Gly Ala Leu His Thr Ala Gly Gln Leu Ala Pro Gly Ser
            780                 785                 790

gcc gac gcc ctg ctg gac tcc gcg cgc gcg gcc ttc acc agc ggc gtg   2570
Ala Asp Ala Leu Leu Asp Ser Ala Arg Ala Ala Phe Thr Ser Gly Val
        795                 800                 805

cag tcc gtc gcc gcc gtc tgc gcc gtg ttc tcc ctg gcg ctc gcc gtc   2618
Gln Ser Val Ala Ala Val Cys Ala Val Phe Ser Leu Ala Leu Ala Val
    810                 815                 820

ctc atc ggc acc cgg ctg cgg gac att tcc gcg atg gac cac ggg cac   2666
Leu Ile Gly Thr Arg Leu Arg Asp Ile Ser Ala Met Asp His Gly His
825                 830                 835                 840

ggc gag gaa ccg gcc gag aac gac gct caa ccg gcc aca tgagcgcact    2715
Gly Glu Glu Pro Ala Glu Asn Asp Ala Gln Pro Ala Thr
                845                 850
```

D8 Cont.

tccggagatg caacggccgc cgtcgaggta tgaggatcac cttccggggt gcacctgcac 2775

ggcaacggag gcgtagtgga gtactggaac agcacggcgg agaccatgcc ccgccaggaa 2835

ctcgaacagt ggaagtggcg caggctccag gccgccatgg accacgccag aaggctttcg 2895

cccttctggc gggaacgact ccccgagaac atcacctcca tggcggacta cgcggcgcgg 2955

gtgcctctcc tgcgcaaggc cgacctcctc gccgcggaag ccgcgtctcc cccttacggc 3015

acctggccct cgctggatcc 3035

<210> 113
<211> 332
<212> PRT
<213> Streptomyces globisporus

<220>
<223> sgcA

<400> 113

```
Met Arg Met Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln Phe
  1               5                  10                  15

Val Arg Ala Thr Leu His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg
             20                  25                  30

Val Thr Val Leu Asp Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu
         35                  40                  45

Thr Ser Val Ala Ala His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr
     50                  55                  60

Val Asp Pro Arg Val Val Asp Glu Val Val Ala Gly His Asp Val Ile
 65                  70                  75                  80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala
                 85                  90                  95

Thr Arg Phe Val Thr Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu
            100                 105                 110

Ala Ala Leu Arg His Gly Val Gly Arg Phe Val His Val Ser Thr Asp
        115                 120                 125

Glu Val Tyr Gly Ser Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro
    130                 135                 140

Leu Ala Pro Asn Val Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu
145                 150                 155                 160


Met Ala Leu Ala Trp His Arg Thr Arg Gly Leu Asp Val Val Val Thr
                165                 170                 175

Arg Cys Thr Asn Asn Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile
            180                 185                 190

Pro Leu Phe Val Thr Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr
        195                 200                 205

Gly Asp Gly Ala His Arg Arg Asp Trp Leu His Val Ser Asp His Cys
    210                 215                 220
```

```
Arg Ala Ile Gln Met Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr
225                 230                 235                 240

His Ile Gly Gly Gly Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu
                245                 250                 255

Leu Leu Thr Ala Cys Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala
            260                 265                 270

Asp Arg Gln Gly His Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile
        275                 280                 285

Arg Gln Glu Leu Gly Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu
    290                 295                 300

Ala Ala Thr Val Lys Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro
305                 310                 315                 320

Leu Lys Glu Ala Ala Gly Leu Leu Asp Ala Val Gly
                325                 330
```

<210> 114
<211> 521
<212> PRT
<213> Streptomyces globisporus

<220>
<223> sgcB

<400> 114

```
Met Thr Ala Val Lys Glu Pro Thr Ser Arg Ala Gly Arg Arg Glu Trp
  1               5                  10                  15

Ile Ala Leu Val Val Leu Ser Leu Pro Thr Met Leu Leu Met Leu Asp
             20                  25                  30

Ile Asn Val Leu Met Leu Ala Leu Pro Gln Leu Ser Glu Asp Leu Gly
         35                  40                  45

Ala Ser Ser Thr Gln Gln Leu Trp Ile Thr Asp Ile Tyr Gly Phe Ala
     50                  55                  60

Ile Ala Gly Phe Leu Val Thr Met Gly Thr Leu Gly Asp Arg Ile Gly
 65                  70                  75                  80

Arg Arg Arg Leu Leu Leu Gly Gly Ala Ala Val Phe Ala Val Val Ser
                 85                  90                  95

Val Val Ala Ala Phe Ser Asp Ser Ala Ala Met Leu Val Val Ser Arg
            100                 105                 110

Ala Val Leu Gly Val Ala Gly Ala Thr Val Met Pro Ser Thr Leu Ala
        115                 120                 125

Leu Ile Ser Asn Met Phe Glu Asp Pro Lys Glu Arg Gly Thr Ala Ile
    130                 135                 140

Ala Met Trp Ala Ser Ala Met Met Ala Gly Val Ala Leu Gly Pro Ala
145                 150                 155                 160

Val Gly Gly Leu Val Leu Ala Ala Phe Trp Trp Gly Ser Val Phe Leu
                165                 170                 175
```

D8 Cont.

Ile Ala Val Pro Val Met Leu Leu Val Val Val Thr Gly Pro Val Leu
180 185 190

Leu Thr Glu Ser Arg Asp Pro Asp Ala Gly Arg Leu Asp Leu Leu Ser
195 200 205

Ala Gly Leu Ser Leu Ala Thr Val Leu Pro Val Ile Tyr Gly Leu Lys
210 215 220

Glu Leu Ala Arg Thr Gly Trp Asp Pro Leu Ala Ala Gly Ala Val Val
225 230 235 240

Leu Gly Val Ile Phe Gly Ala Leu Phe Val Gln Arg Gln Arg Arg Leu
245 250 255

Ala Asp Pro Met Leu Asp Leu Gly Leu Phe Ala Asp Arg Thr Leu Arg
260 265 270

Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile Met Gly Gly Thr
275 280 285

Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala Gly His Ser Pro
290 295 300

Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys Met Leu Val Val
305 310 315 320

Gly Val Gln Leu Ser Asn Leu Leu Ala Gln Arg Met Pro Pro Ser Arg
325 330 335

Val Leu Leu Gly Gly Leu Leu Ile Ala Ala Val Gly Gln Leu Leu Ile
340 345 350

Thr Gln Val Asp Thr Glu Asp Thr Ala Leu Leu Ile Ala Ala Thr Thr
355 360 365

Leu Ile Tyr Phe Gly Ala Ser Pro Val Gly Pro Ile Thr Thr Gly Ala
370 375 380

Ile Met Gly Ala Ala Pro Pro Glu Lys Ala Gly Ala Ala Ser Ser Leu
385 390 395 400

D8 Cont.

Ser Ala Thr Gly Gly Glu Phe Gly Val Ala Leu Gly Ile Ala Gly Leu
405 410 415

Gly Ser Leu Gly Thr Val Val Tyr Ser Ala Gly Val Glu Val Pro Asp
420 425 430

Ala Ala Gly Pro Ala Asp Ala Asp Ala Ala Gln Glu Ser Ile Ala Gly
435 440 445

Ala Leu His Thr Ala Gly Gln Leu Ala Pro Gly Ser Ala Asp Ala Leu
450 455 460

Leu Asp Ser Ala Arg Ala Ala Phe Thr Ser Gly Val Gln Ser Val Ala
465 470 475 480
Ala Val Cys Ala Val Phe Ser Leu Ala Leu Ala Val Leu Ile Gly Thr
485 490 495

Arg Leu Arg Asp Ile Ser Ala Met Asp His Gly His Gly Glu Glu Pro
500 505 510

Ala Glu Asn Asp Ala Gln Pro Ala Thr
515 520

<210> 115
<211> 329
<212> PRT
<213> Saccharopolyspora erythraea

<400> 115
Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Tyr
1 5 10 15

Val Arg Gln Leu Leu Gly Gly Ala Tyr Pro Ala Phe Ala Gly Ala Asp
20 25 30

Val Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Glu Glu Asn Leu
35 40 45

Arg Pro Val Ala Asp Asp Pro Arg Phe Arg Phe Val Arg Gly Asp Ile
50 55 60

Cys Glu Trp Asp Val Val Ser Glu Val Met Arg Glu Val Asp Val Val
65 70 75 80

Val His Phe Ala Ala Glu Thr His Val Asp Arg Ser Ile Leu Gly Ala
85 90 95

Ser Asp Phe Val Val Thr Asn Val Val Gly Thr Asn Thr Leu Leu Gln
100 105 110

Gly Ala Leu Ala Ala Asn Val Ser Lys Phe Val His Val Ser Thr Asp
115 120 125

Glu Val Tyr Gly Thr Ile Glu His Gly Ser Trp Pro Glu Asp His Leu
130 135 140

Leu Glu Pro Asn Ser Pro Tyr Ser Ala Ala Lys Ala Gly Ser Asp Leu
145 150 155 160

Ile Ala Arg Ala Tyr His Arg Thr His Gly Leu Pro Val Cys Ile Thr
165 170 175

Arg Cys Ser Asn Asn Tyr Gly Pro Tyr Gln Phe Pro Glu Lys Val Leu
180 185 190

Pro Leu Phe Ile Thr Asn Leu Met Asp Gly Arg Arg Val Pro Leu Tyr
195 200 205

Gly Asp Gly Leu Asn Val Arg Asp Trp Leu His Val Thr Asp His Cys
210 215 220

Arg Gly Ile Gln Leu Val Ala Glu Ser Gly Arg Ala Gly Glu Ile Tyr
225 230 235 240

Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Lys Glu Leu Thr Glu Arg
245 250 255

Val Leu Glu Leu Met Gly Gln Asp Trp Ser Met Val Gln Pro Val Thr
260 265 270

Asp Arg Lys Gly His Asp Arg Arg Tyr Ser Val Asp His Thr Lys Ile
275 280 285

D8 Cont.

```
Ser Glu Glu Leu Gly Tyr Glu Pro Val Val Pro Phe Glu Arg Gly Leu
    290                 295                 300

Ala Glu Thr Ile Glu Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
305                 310                 315                 320

Leu Lys Ser Ala Pro Asp Gly Gly Lys
                325
```

<210> 116
<211> 333
<212> PRT
<213> Streptomyces fradiae

<400> 116

```
Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Phe
  1               5                  10                  15

Thr Gly Gln Leu Leu Thr Gly Ala Tyr Pro Asp Leu Gly Ala Thr Arg
            20                  25                  30

Thr Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Pro Ala Asn Leu
        35                  40                  45

Glu His Val Ala Gly His Pro Asp Leu Glu Phe Val Arg Gly Asp Ile
    50                  55                  60

Ala Asp His Gly Trp Trp Arg Arg Leu Met Glu Gly Val Gly Leu Val
65                  70                  75                  80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Glu Ser Ser
                85                  90                  95

Glu Ala Phe Val Arg Thr Asn Val Glu Gly Thr Arg Val Leu Leu Gln
            100                 105                 110

Ala Ala Val Asp Ala Gly Val Gly Arg Phe Val His Ile Ser Thr Asp
        115                 120                 125

Glu Val Tyr Gly Ser Ile Ala Glu Gly Ser Trp Pro Glu Asp His Pro
    130                 135                 140

Val Ala Pro Asn Ser Pro Tyr Ala Ala Thr Lys Lys Ala Ser Asp Leu
145                 150                 155                 160

Leu Ala Leu Ala Tyr His Arg Thr Tyr Gly Leu Asp Val Arg Val Thr
                165                 170                 175

Arg Cys Ser Asn Asn Tyr Gly Pro Arg Gln Tyr Pro Glu Lys Ala Val
            180                 185                 190

Pro Leu Phe Thr Thr Asn Leu Leu Asp Gly Leu Pro Val Pro Leu Tyr
        195                 200                 205

Gly Asp Gly Gly Asn Thr Arg Glu Trp Leu His Val Asp Asp His Cys
    210                 215                 220

Arg Gly Val Ala Leu Val Gly Ala Gly Gly Arg Pro Gly Val Ile Tyr
225                 230                 235                 240

Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Ala Glu Leu Thr Asp Arg
                245                 250                 255
```

D8 Cont'

```
Ile Leu Glu Leu Cys Gly Ala Asp Arg Ser Ala Leu Arg Arg Val Ala
            260                 265                 270

Asp Arg Pro Gly His Asp Arg Arg Tyr Ser Val Asp Thr Thr Lys Ile
        275                 280                 285

Arg Glu Glu Leu Gly Tyr Ala Pro Arg Thr Gly Ile Thr Glu Gly Leu
    290                 295                 300

Ala Gly Thr Val Ala Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
305                 310                 315                 320

Leu Lys Arg Ser Pro Gly Gly Arg Glu Leu Glu Arg Ala
                325                 330
```

<210> 117
<211> 331
<212> PRT
<213> Streptomyces argillaceus

<400> 117

```
Met Thr Thr Thr Ser Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly
  1               5                  10                  15

Ser His Tyr Val Arg Thr Leu Leu Gly Pro Arg Gly Val Pro Asp Val
             20                  25                  30

Thr Val Thr Val Leu Asp Lys Leu Thr Tyr Ala Gly Thr Leu Thr Asn
         35                  40                  45

Leu Ala Glu Val Ser Asp Ser Asp Arg Phe Arg Phe Val Arg Gly Asp
     50                  55                  60

Ile Cys Asp Ala Pro Leu Val Asp Asp Leu Leu Ala Val His Asp Gln
 65                  70                  75                  80

Val Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Leu Gly
                 85                  90                  95

Ala Ala Asp Phe Val Arg Thr Asn Val Thr Gly Thr Gln Thr Leu Leu
            100                 105                 110

Asp Ala Ala Leu Arg Gln Gly Ile Glu Thr Phe Val His Ile Ser Thr
        115                 120                 125

Asp Glu Val Tyr Gly Ser Ile Asp Ala Gly Ser Trp Pro Glu Thr Ala
    130                 135                 140

Pro Val Ser Pro Asn Ser Leu Tyr Ser Ala Ala Lys Ala Ser Ser Asp
145                 150                 155                 160

Leu Val Ala Leu Ala Tyr His Arg Thr His Gly Leu Asp Val Arg Val
                165                 170                 175

Thr Arg Cys Ser Asn Asn Tyr Gly Ser His Gln Phe Pro Glu Lys Val
            180                 185                 190

Ile Pro Leu Phe Val Thr Ser Leu Leu Asp Gly Arg Glu Val Pro Leu
        195                 200                 205

Tyr Gly Asp Gly Thr Asn Val Arg Asp Trp Leu His Val Asp Asp His
    210                 215                 220
```

D8 Cont.

Val Arg Ala Ile Glu Leu Val Arg Thr Gly Gly Arg Ala Gly Glu Val
225 230 235 240

Tyr Asn Ile Gly Gly Gly Thr Glu Leu Ser Asn Lys Glu Leu Thr Gln
245 250 255

Leu Leu Leu Asp Ala Cys Gly Ala Gly Trp Asp Arg Val Arg Tyr Val
260 265 270

Thr Asp Arg Lys Gly His Asp Arg Arg Tyr Ser Val Asp Cys Thr Lys
275 280 285

Ile Arg Arg Glu Leu Gly Tyr Arg Pro Ala Arg Glu Phe Gly Asp Ala
290 295 300

Leu Ala Glu Thr Val Ala Trp Tyr Arg His His Arg Ala Trp Trp Glu
305 310 315 320

Pro Leu Thr Arg Ala Tyr Gly Ala Val Ala Ala
325 330

<210> 118
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6-His tag

<400> 118
His His His His His His
1 5

<210> 119
<211> 256

<212> PRT

D8
Cont

<213> Artificial

<220>

<223> Computed consensus sequence.

<400> 1

Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Tyr
1 5 10 15

Val Arg Ile Leu Gly Pro Ala Val Val Leu Asp Lys Leu Thr Tyr Ala
20 25 30

Gly Asn Asn Leu Val Ala Pro Arg Phe Phe Val Arg Gly Asp Ile Asp
35 40 45

Val Val Glu Val Met Asp Val Val Val His Phe Ala Ala Glu Ser His
50 55 60

Val Asp Arg Ser Ile Ala Phe Val Thr Asn Val Gly Thr Asn Thr Leu
65 70 75 80

```
Leu Ala Ala Leu Gly Val Lys Phe Val His Val Ser Thr Asp Glu Val
                85                  90                  95

Tyr Gly Ser Ile Gly Ser Trp Pro Glu Asp Pro Leu Pro Asn Ser Pro
            100                 105                 110

Tyr Ala Lys Ala Gly Ser Asp Leu Ile Ala Leu Ala Tyr His Arg Thr
        115                 120                 125

His Gly Leu Asp Val Val Thr Arg Cys Ser Asn Asn Tyr Gly Pro Gln
    130                 135                 140

Phe Pro Glu Lys Val Leu Pro Leu Phe Ile Thr Asn Leu Leu Asp Gly
145                 150                 155                 160

Val Pro Leu Tyr Gly Asp Gly Asn Arg Asp Trp Leu His Val Asp His
                165                 170                 175

Cys Arg Gly Ile Leu Val Gly Arg Ala Gly Glu Ile Tyr Asn Ile Gly
            180                 185                 190

Gly Gly Thr Glu Leu Thr Asn Glu Leu Thr Val Leu Glu Cys Gly Asp
        195                 200                 205

Trp Ser Val Val Asp Arg Gly His Asp Arg Arg Tyr Ser Val Asp Thr
    210                 215                 220

Lys Ile Arg Glu Leu Gly Tyr Pro Phe Glu Gly Leu Ala Thr Val Trp
225                 230                 235                 240

Tyr Arg Asp Asn Arg Ala Trp Trp Glu Leu Pro Leu Lys Ala Gly Gly
                245                 250                 255
```